

SEQUENCE LISTING

<110> Garvan Institute of Medical Research

<120> Method of modulating bone growth, remodeling and adiposity

<130> 42-000400US

<160> 20

<170> PatentIn version 3.3

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<212> DNA

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<222> (7)..(1161)

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Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala Tyr Gly
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Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile
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Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Ala Met
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Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile
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Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn
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Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr
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Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg
Page 3

195

200

205

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Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr Arg Lys Ala Phe
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gag ttc ctg gca gat aag gtg gtc tgt acc gag tcc tgg cca ctg gct Glu Phe Leu Ala Asp Lys Val Val Cys Thr Glu Ser Trp Pro Leu Ala 195 200 205	1283
cac cac cgc acc atc tac acc acc ttc ctg ctc ctc ttc cag tac tgc His His Arg Thr Ile Tyr Thr Thr Phe Leu Leu Leu Phe Gln Tyr Cys 210 215 220	1331
ctc cca ctg ggc ttc atc ctg gtc tgt tat gca cgc atc tac cgg cgc Leu Pro Leu Gly Phe Ile Leu Val Cys Tyr Ala Arg Ile Tyr Arg Arg 225 230 235 240	1379
ctg cag agg cag ggg cgc gtg ttt cac aag ggc acc tac agc ttg cga Leu Gln Arg Gln Gly Arg Val Phe His Lys Gly Thr Tyr Ser Leu Arg 245 250 255	1427
gct ggg cac atg aag cag gtc aat gtg gtg ctg gtg gtg atg gtg gtg Ala Gly His Met Lys Gln Val Asn Val Val Leu Val Val Met Val Val 260 265 270	1475
gcc ttt gcc gtg ctc tgg ctg cct ctg cat gtg ttc aac agc ctg gaa Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Ser Leu Glu 275 280 285	1523
gac tgg cac cat gag gcc atc ccc atc tgc cac ggg aac ctc atc ttc Asp Trp His His Glu Ala Ile Pro Ile Cys His Gly Asn Leu Ile Phe 290 295 300	1571
tta gtg tgc cac ttg ctt gcc atg gcc tcc acc tgc gtc aac cca ttc Leu Val Cys His Leu Leu Ala Met Ala Ser Thr Cys Val Asn Pro Phe 305 310 315 320	1619
atc tat ggc ttt ctc aac acc aac ttc aag aag gag atc aag gcc ctg Ile Tyr Gly Phe Leu Asn Thr Asn Phe Lys Lys Glu Ile Lys Ala Leu 325 330 335	1667
gtg ctg act tgc cag cag agc gcc ccc ctg gag gag tcg gag cat ctg Val Leu Thr Cys Gln Gln Ser Ala Pro Leu Glu Glu Ser Glu His Leu 340 345 350	1715
ccc ctg tcc aca gta cat acg gaa gtc tcc aaa ggg tcc ctg agg cta Pro Leu Ser Thr Val His Thr Glu Val Ser Lys Gly Ser Leu Arg Leu 355 360 365	1763
agt ggc agg tcc aat ccc att taa ccaggtctag gtcttctccc tgccatgtcc Ser Gly Arg Ser Asn Pro Ile 370 375	1817
cttgccaggc tcttccactt agctaagtgg gcacactgca agctgggggtg gcaccccgagc	1877
attcctgggt tctctggggtc cagataggct ggcaagagct gtttttgcatt ccatttgcatt	1937

cgtgaagact ggcattttga tacttcagct gtttgttcct gggagaattc tgagcacaga 1997
 ttccagaggt cacagtaagc cttgcagctt gagctgaaag atgccagagc cggagatgtc 2057
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 cagggatttc acctccacca gtgagaccac ggggccactg tggggtgagg gaaggagcgc 2177
 ttggagtcag agctctagac cttggtcaac tcttcacctc tgtgagagat ggtgtgtgga 2237
 ggtgcttcag aagtaaagaa ttc 2260

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<400> 6

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Gly Glu Asn Arg Ser Lys Pro Leu Gly Thr Pro Tyr Asn Phe Ser Glu
 20 25 30

His Cys Gln Asp Ser Val Asp Val Met Val Phe Ile Val Thr Ser Tyr
 35 40 45

Ser Ile Glu Thr Val Val Gly Val Leu Gly Asn Leu Cys Leu Met Cys
 50 55 60

Val Thr Val Arg Gln Lys Glu Lys Ala Asn Val Thr Asn Leu Leu Ile
 65 70 75 80

Ala Asn Leu Ala Phe Ser Asp Phe Leu Met Cys Leu Leu Cys Gln Pro
 85 90 95

Leu Thr Ala Val Tyr Thr Ile Met Asp Tyr Trp Ile Phe Gly Glu Thr
 100 105 110

Leu Cys Lys Met Ser Ala Phe Ile Gln Cys Met Ser Val Thr Val Ser
 115 120 125

Ile Leu Ser Leu Val Leu Val Ala Leu Glu Arg His Gln Leu Ile Ile
 130 135 140

Asn Pro Thr Gly Trp Lys Pro Ser Ile Ser Gln Ala Tyr Leu Gly Ile
 145 150 155 160

Val Leu Ile Trp Val Ile Ala Cys Val Leu Ser Leu Pro Phe Leu Ala
165 170 175

Asn Ser Ile Leu Glu Asn Val Phe His Lys Asn His Ser Lys Ala Leu
180 185 190

Glu Phe Leu Ala Asp Lys Val Val Cys Thr Glu Ser Trp Pro Leu Ala
195 200 205

His His Arg Thr Ile Tyr Thr Thr Phe Leu Leu Leu Phe Gln Tyr Cys
210 215 220

Leu Pro Leu Gly Phe Ile Leu Val Cys Tyr Ala Arg Ile Tyr Arg Arg
225 230 235 240

Leu Gln Arg Gln Gly Arg Val Phe His Lys Gly Thr Tyr Ser Leu Arg
245 250 255

Ala Gly His Met Lys Gln Val Asn Val Val Leu Val Val Met Val Val
260 265 270

Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Ser Leu Glu
275 280 285

Asp Trp His His Glu Ala Ile Pro Ile Cys His Gly Asn Leu Ile Phe
290 295 300

Leu Val Cys His Leu Leu Ala Met Ala Ser Thr Cys Val Asn Pro Phe
305 310 315 320

Ile Tyr Gly Phe Leu Asn Thr Asn Phe Lys Lys Glu Ile Lys Ala Leu
325 330 335

Val Leu Thr Cys Gln Gln Ser Ala Pro Leu Glu Glu Ser Glu His Leu
340 345 350

Pro Leu Ser Thr Val His Thr Glu Val Ser Lys Gly Ser Leu Arg Leu
355 360 365

Ser Gly Arg Ser Asn Pro Ile
370 375

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<211> 1423
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<213> human neuropeptide Y5 receptor

<220>

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<222> (71)..(1408)

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agactataat atg gat tta gag ctc gag gag tat tat aac aag aca ctt 109
Met Asp Leu Glu Leu Asp Glu Tyr Tyr Asn Lys Thr Leu
1 5 10

gcc aca gag aat aat act gct gcc act cgg aat tct gat ttc cca gtc 157
Ala Thr Glu Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val
15 20 25

tgg gat gac tat aaa agc agt gta gat gac tta cag tat ttt ctg att 205
Trp Asp Asp Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile
30 35 40 45

ggg ctc tat aca ttt gta agt ctt ctt ggc ttt atg ggg aat cta ctt 253
Gly Leu Tyr Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu
50 55 60

att tta atg gct ctc atg aaa aag cgt aat cag aag act acg gta aac 301
Ile Leu Met Ala Leu Met Lys Lys Arg Asn Gln Lys Thr Thr Val Asn
65 70 75

ttc ctc ata ggc aat ctg gcc ttt tct gat atc ttg gtt gtg ctg ttt 349
Phe Leu Ile Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe
80 85 90

tgc tca cct ttc aca ctg acg tct gtc ttg ctg gat cag tgg atg ttt 397
Cys Ser Pro Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe
95 100 105

ggc aaa gtc atg tgc cat att atg cct ttt ctt caa tgt gtg tca gtt 445
Gly Lys Val Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val
110 115 120 125

ttg gtt tca act tta att tta ata tca att gcc att gtc agg tat cat 493
Leu Val Ser Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His
130 135 140

atg ata aaa cat ccc ata tct aat aat tta aca gca aac cat ggc tac 541
Met Ile Lys His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr
145 150 155

ttt ctg ata gct act gtc tgg aca cta ggt ttt gcc atc tgt tct ccc 589
Phe Leu Ile Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro
160 165 170

ctt cca gtg ttt cac agt ctt gtg gaa ctt caa gaa aca ttt ggt tca 637
Leu Pro Val Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Gly Ser
175 180 185

gca ttg ctg agc agc agg tat tta tgt gtt gag tca tgg cca tct gat 685
Ala Leu Leu Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp

190	195	200	205	
tca tac aga att gcc ttt act atc tct tta ttg cta gtt cag tat att				733
Ser Tyr Arg Ile	Ala Phe Thr Ile	Ser Leu Leu Val	Gln Tyr Ile	
	210	215	220	
ctg ccc tta gtt tgt ctt act gta agt cat aca agt gtc tgc aga agt				781
Leu Pro Leu Val Cys Leu Thr Val Ser His Thr Ser Val Cys Arg Ser				
	225	230	235	
ata agc tgt gga ttg tcc aac aaa gaa aac aga ctt gaa gaa aat gag				829
Ile Ser Cys Gly Leu Ser Asn Lys Glu Asn Arg Leu Glu Glu Asn Glu				
	240	245	250	
atg atc aac tta act ctt cat cca tcc aaa aag agt ggg cct cag gtg				877
Met Ile Asn Leu Thr Leu His Pro Ser Lys Lys Ser Gly Pro Gln Val				
	255	260	265	
aaa ctc tct ggc agc cat aaa tgg agt tat tca ttc atc aaa aaa cac				925
Lys Leu Ser Gly Ser His Lys Trp Ser Tyr Ser Phe Ile Lys Lys His				
	270	275	280	285
aga aga aga tat agc aag aag aca gca tgt gtg tta cct gct cca gaa				973
Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala Pro Glu				
	290	295	300	
aga cct tct caa gag aac cac tcc aga ata ctt cca gaa aac ttt ggc				1021
Arg Pro Ser Gln Glu Asn His Ser Arg Ile Leu Pro Glu Asn Phe Gly				
	305	310	315	
tct gta aga agt cag ctc tct tca tcc agt aag ttc ata cca ggg gtc				1069
Ser Val Arg Ser Gln Leu Ser Ser Ser Ser Lys Phe Ile Pro Gly Val				
	320	325	330	
ccc act tgc ttt gag ata aaa cct gaa gaa aat tca gat gtt cat gaa				1117
Pro Thr Cys Phe Glu Ile Lys Pro Glu Glu Asn Ser Asp Val His Glu				
	335	340	345	
ttg aga gta aaa cgt tct gtt aca aga ata aaa aag aga tct cga agt				1165
Leu Arg Val Lys Arg Ser Val Thr Arg Ile Lys Lys Arg Ser Arg Ser				
	350	355	360	365
gtt ttc tac aga ctg acc ata ctg ata tta gta ttt gct gtt agt tgg				1213
Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp				
	370	375	380	
atg cca cta cac ctt ttc cat gtg gta act gat ttt aat gac aat ctt				1261
Met Pro Leu His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu				
	385	390	395	
att tca aat agg cat ttc aag ttg gtg tat tgc att tgt cat ttg ttg				1309
Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu				
	400	405	410	
ggc atg atg tcc tgt tgt ctt aat cca att cta tat ggg ttt ctt aat				1357
Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn				
	415	420	425	
aat ggg att aaa gct gat tta gtg tcc ctt ata cac tgt ctt cat atg				1405
Asn Gly Ile Lys Ala Asp Leu Val Ser Leu Ile His Cys Leu His Met				

430	435	440	445	
taa taattctcac tgttt				1423

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Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val Trp Asp Asp
20 25 30

Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr
35 40 45

Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met
50 55 60

Ala Leu Met Lys Lys Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile
65 70 75 80

Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro
85 90 95

Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val
100 105 110

Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser
115 120 125

Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys
130 135 140

His	Pro	Ile	Ser	Asn	Asn	Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile
145					150					155					160

Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val
165 170 175

Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu
180 185 190

Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg
 195 200 205

Ile Ala Phe Thr Ile Ser Leu Leu Val Gln Tyr Ile Leu Pro Leu
 210 215 220

Val Cys Leu Thr Val Ser His Thr Ser Val Cys Arg Ser Ile Ser Cys
 225 230 235 240

Gly Leu Ser Asn Lys Glu Asn Arg Leu Glu Glu Asn Glu Met Ile Asn
 245 250 255

Leu Thr Leu His Pro Ser Lys Lys Ser Gly Pro Gln Val Lys Leu Ser
 260 265 270

Gly Ser His Lys Trp Ser Tyr Ser Phe Ile Lys Lys His Arg Arg Arg
 275 280 285

Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala Pro Glu Arg Pro Ser
 290 295 300

Gln Glu Asn His Ser Arg Ile Leu Pro Glu Asn Phe Gly Ser Val Arg
 305 310 315 320

Ser Gln Leu Ser Ser Ser Ser Lys Phe Ile Pro Gly Val Pro Thr Cys
 325 330 335

Phe Glu Ile Lys Pro Glu Glu Asn Ser Asp Val His Glu Leu Arg Val
 340 345 350

Lys Arg Ser Val Thr Arg Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr
 355 360 365

Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro Leu
 370 375 380

His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn
 385 390 395 400

Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly Met Met
 405 410 415

Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile
 420 425 430

Lys Ala Asp Leu Val Ser Leu Ile His Cys Leu His Met
 435 440 445

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 <212> DNA
 <213> human neuropeptide Y7 receptor

<220>
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 <222> (369)..(1595)

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 tggctctccat ctcccgacct cgtgatccac ccacctcggc ctcccaaagt gctgggatta 180
 caggcgtgag accgcgcccg gccaatctcc tttcttagtt gcctctgccc acctcttctc 240
 ttctgcttcc atattacagg tttcctcagt tgcgaaatta ggatgttaat tatagctttt 300
 gacatacaag aaacatcaaa aagattgaat gtcttaataa gagtgaagca tgtagatcag 360
 tgactgct atg ttc atc atg aat gag aaa tgg gac aca aac tct tca gaa 410
 Met Phe Ile Met Asn Glu Lys Trp Asp Thr Asn Ser Ser Glu
 1 5 10
 aac tgg cat ccc atc tgg aat gtc aat gac aca aag cat cat ctg tac 458
 Asn Trp His Pro Ile Trp Asn Val Asn Asp Thr Lys His His Leu Tyr
 15 20 25 30
 tca gat att aat att acc tat gtg aac tac tat ctt cac cag cct caa 506
 Ser Asp Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln
 35 40 45
 gtg gca gca atc ttc att att tcc tac ttt ctg atc ttc ttt ttg tgc 554
 Val Ala Ala Ile Phe Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys
 50 55 60
 atg atg gga aat act gtg gtt tgc ttt att gta atg agg aac aaa cat 602
 Met Met Gly Asn Thr Val Val Cys Phe Ile Val Met Arg Asn Lys His
 65 70 75
 atg cac aca gtc act aat ctc ttc atc tta aac ctg gcc ata agt gat 650
 Met His Thr Val Thr Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp
 80 85 90
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 Leu Leu Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile
 95 100 105 110
 ata gca gga tgg cca ttt gga aac acg atg tgc aag atc agt gga ttg 746
 Ile Ala Gly Trp Pro Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu
 115 120 125
 gtc cag gga ata tct gtc gca gct tca gtc ttt acg tta gtt gca att 794

Val Gln Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile	
130 135 140	
gct gta gat agg ttc cag tgt gtg gtc tac cct ttt aaa cca aag ctc	842
Ala Val Asp Arg Phe Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu	
145 150 155	
act atc aag aca gcg ttt gtc att att atg atc atc tgg gtc cta gcc	890
Thr Ile Lys Thr Ala Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala	
160 165 170	
atc acc att atg tct cca tct gca gta atg tta cat gtg caa gaa gaa	938
Ile Thr Ile Met Ser Pro Ser Ala Val Met Leu His Val Gln Glu Glu	
175 180 185 190	
aaa tat tac cga gtg aga ctc aac tcc cag aat aaa acc agt cca gtc	986
Lys Tyr Tyr Arg Val Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val	
195 200 205	
tac tgg tgc cgg gaa gac tgg cca aat cag gaa atg agg aag atc tac	1034
Tyr Trp Cys Arg Glu Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr	
210 215 220	
acc act gtg ctg ttt gcc aac atc tac ctg gct ccc ctc tcc ctc att	1082
Thr Thr Val Leu Phe Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile	
225 230 235	
gtc atc atg tat gga agg att gga att tca ctc ttc agg gct gca gtt	1130
Val Ile Met Tyr Gly Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val	
240 245 250	
cct cac aca ggc agg aag aac cag gag cag tgg cac gtg gtg tcc agg	1178
Pro His Thr Gly Arg Lys Asn Gln Glu Gln Trp His Val Val Ser Arg	
255 260 265 270	
aag aag cag aag atc att aag atg ctc ctg att gtg gcc ctg ctt ttt	1226
Lys Lys Gln Lys Ile Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe	
275 280 285	
att ctc tca tgg ctg ccc ctg tgg act cta atg atg ctc tca gac tac	1274
Ile Leu Ser Trp Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr	
290 295 300	
gct gac ctt tct cca aat gaa ctg cag atc atc aac atc tac atc tac	1322
Ala Asp Leu Ser Pro Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr	
305 310 315	
cct ttt gca cac tgg ctg gca ttc ggc aac agc agt gtc aat ccc atc	1370
Pro Phe Ala His Trp Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile	
320 325 330	
att tat ggt ttc ttc aac gag aat ttc cgc cgt ggt ttc caa gaa gct	1418
Ile Tyr Gly Phe Phe Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala	
335 340 345 350	
ttc cag ctc cag ctc tgc caa aaa aga gca aag cct atg gaa gct tat	1466
Phe Gln Leu Gln Leu Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr	
355 360 365	
acc cta aaa gct aaa agc cat gtg ctc ata aac aca tct aat cag ctt	1514

Thr Leu Lys Ala Lys Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu
 370 375 380
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 Val Gln Glu Ser Thr Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr
 385 390 395
 agg aaa agt gct gaa aac ccc aac agg aat tag tgatggaaga attaaaagaa 1615
 Arg Lys Ser Ala Glu Asn Pro Asn Arg Asn
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 ctaaataaaaa catttactga aagccctctc tggcaaaaaa attaaaaata aacaaaaatg 1795
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 <212> PRT
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<400> 10

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His Pro Ile Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp
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Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala
 35 40 45

Ala Ile Phe Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met
 50 55 60

Gly Asn Thr Val Val Cys Phe Ile Val Met Arg Asn Lys His Met His
 65 70 75 80

Thr Val Thr Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu
 85 90 95

Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala
 100 105 110

Gly Trp Pro Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu Val Gln
 115 120 125

Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val
 130 135 140

Asp Arg Phe Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile
 145 150 155 160

Lys Thr Ala Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr
 165 170 175

Ile Met Ser Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr
 180 185 190

Tyr Arg Val Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp
 195 200 205

Cys Arg Glu Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr
 210 215 220

Val Leu Phe Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile
 225 230 235 240

Met Tyr Gly Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His
 245 250 255

Thr Gly Arg Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys
 260 265 270

Gln Lys Ile Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu
 275 280 285

Ser Trp Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp
 290 295 300

Leu Ser Pro Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe
 305 310 315 320

Ala His Trp Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr
 325 330 335

Gly Phe Phe Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln
 340 345 350

Leu Gln Leu Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Thr Leu
 355 360 365

Lys Ala Lys Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln
 370 375 380

Glu Ser Thr Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys
 385 390 395 400

Ser Ala Glu Asn Pro Asn Arg Asn
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<210> 11
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 <213> mouse neuropeptide Y1 receptor

<220>
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 caaaacataa aaaa atg aac tca act ctg ttc tcc aag gtt gaa aat cac 170
 Met Asn Ser Thr Leu Phe Ser Lys Val Glu Asn His
 1 5 10
 tca att cac tat aat gcc tca gag aat tct cca ctt ctg gct ttt gaa 218
 Ser Ile His Tyr Asn Ala Ser Glu Asn Ser Pro Leu Leu Ala Phe Glu
 15 20 25
 aat gat gac tgc cac ctg ccc ttg gct gtg ata ttc acc ttg gct ctc 266
 Asn Asp Asp Cys His Leu Pro Leu Ala Val Ile Phe Thr Leu Ala Leu
 30 35 40
 gct tat ggg gcg gtg att att ctt ggc gtc tct gga aac ctg gca ttg 314
 Ala Tyr Gly Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu
 45 50 55 60
 atc ata atc att ctg aaa cag aag gag atg aga aat gtc acc aac att 362
 Ile Ile Ile Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile
 65 70 75
 ctg atc gtg aac ctc tcc ttc tca gac ttg ctc gtt gcg gtc atg tgt 410
 Leu Ile Val Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys
 80 85 90
 ctc ccg ttc act ttt gta tat aca ctg atg gac cac tgg gtc ttc ggg 458
 Leu Pro Phe Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly
 95 100 105
 gag acc atg tgc aaa ctg aat ccc ttt gta cag tgt gtc tcc atc aca 506
 Glu Thr Met Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr
 110 115 120

gta tcc att ttc tcg ctg gtt ctc atc gct gtg gaa cgg cat cag cta Val Ser Ile Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu 125 130 135 140	554
atc atc aac cca aga ggg tgg aga cca aac aat aga cat gct tac ata Ile Ile Asn Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile 145 150 155	602
ggc att act gtc att tgg gtc ctt gca gtg gct tct tct ctg ccc ttt Gly Ile Thr Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe 160 165 170	650
gtg atc tat caa att ctg acc gac gag ccc ttc caa aat gtg tca ctt Val Ile Tyr Gln Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu 175 180 185	698
gcg gcg ttc aag gac aag tat gtg tgc ttt gac aaa ttc cca tct gac Ala Ala Phe Lys Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp 190 195 200	746
tct cac agg ctg tct tac acg act ctc ctc ctg gtg ctg cag tat ttc Ser His Arg Leu Ser Tyr Thr Thr Leu Leu Val Leu Gln Tyr Phe 205 210 215 220	794
ggc cca ctc tgc ttt ata ttc ata tgc tac ttc aag ata tac att cgc Gly Pro Leu Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg 225 230 235	842
ttg aaa agg aga aac aac atg atg gac aag atc cgg gac agt aag tac Leu Lys Arg Arg Asn Asn Met Met Asp Lys Ile Arg Asp Ser Lys Tyr 240 245 250	890
agg tcc agt gag acc aag cga atc aac atc atg ctg ctc tcc att gtg Arg Ser Ser Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val 255 260 265	938
gtc gcc ttc gcc gtc tgc tgg ctg ccc ctt acc atc ttc aac act gtg Val Ala Phe Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val 270 275 280	986
ttc gac tgg aac cac cag atc att gcc acc tgc aac cac aat ctg ctg Phe Asp Trp Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu 285 290 295 300	1034
ttt ctg ctc tgt cac ctc acc gcc atg atc tcc acc tgc gtc aac ccc Phe Leu Leu Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro 305 310 315	1082
atc ttt tat gga ttc ctg aac aaa aat ttc cag aga gac ttg cag ttc Ile Phe Tyr Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe 320 325 330	1130
ttc ttc aac ttt tgt gac ttc cgg tct cga gac gat gac tac gag acc Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr 335 340 345	1178
ata gcc atg tct acc atg cat acg gat gtg tcc aag acg tct ctg aag Ile Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys 350 355 360	1226

cag gct agc cca gtc gca ttt aaa aaa atc agt atg aat gac aat gaa 1274
 Gln Ala Ser Pro Val Ala Phe Lys Lys Ile Ser Met Asn Asp Asn Glu
 365 370 375 380

aaa gtc tga agctgtcag agcatatggt cccaggccat atctgtggaa 1323
 Lys Val

aaacaagcac agcctgccgc atgcttttctt tacctatgct ctgggggaac ggaatgaggc 1383

gcgcttggaag agcccaggac atctgtgtta aatttgactg cttttgatgg ttgccctgat 1443

tacttagaaa tctagattac tttgtaatct atctctggca acagttttga ctagatgtcc 1503

tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg 1563

cgcgcgcgcg cgcgcacgtg caaaagagaa agagagagag agaaggagag agacagacag 1623

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caaagagttt tacatttgtt ttgttgaggat gaatttctct gaagtaatgt catgagctca 1743

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<212> PRT

<213> mouse neuropeptide Y1 receptor

<400> 12

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Asn Ala Ser Glu Asn Ser Pro Leu Leu Ala Phe Glu Asn Asp Asp Cys
 20 25 30

His Leu Pro Leu Ala Val Ile Phe Thr Leu Ala Leu Ala Tyr Gly Ala
 35 40 45

Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile Ile
 50 55 60

Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val Asn
 65 70 75 80

Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys Leu Pro Phe Thr
 85 90 95

Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Thr Met Cys
100 105 110
Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile Phe
115 120 125
Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn Pro
130 135 140
Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile Gly Ile Thr Val
145 150 155 160
Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Val Ile Tyr Gln
165 170 175
Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu Ala Ala Phe Lys
180 185 190
Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp Ser His Arg Leu
195 200 205
Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys
210 215 220
Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg Arg
225 230 235 240
Asn Asn Met Met Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Glu
245 250 255
Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe Ala
260 265 270
Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp Asn
275 280 285
His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu Cys
290 295 300
His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr Gly
305 310 315 320
Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe
325 330 335

Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser
 340 345 350

Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro
 355 360 365

Val Ala Phe Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Val
 370 375 380

<210> 13
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 cattctagtt ggtgacttcc agaccagtga gaaggcctgt ctcaaaaaac aatgtggatg 120
 gcacctgagg aatgatacct gagggttgct tttgactata gacacagatg ttcacactga 180
 accacccaca ccccccccca cacacacacc agaggggggg ggggcttatg tgcacaagaa 240
 gtgaaagaaa aaagggctgt gtgagaatcc agctgttttg ccttatttta atctcccaaa 300
 gatcaggtgc tcagcacatg cagatgtttg cccctttgtt atattttagg ctgctgtata 360
 cttacacatt tcaaacaatt aagtgggtga cactttcctt taagttaatg tgttgacttc 420
 atagcaatta taaaattgat aaactttatt gcattcattt tgcattaaaa tgggaatttat 480
 ttgatctcac tcattgtgga gctgattctc tctctaacag gaaagtgtag ttttgtcatg 540
 atcatagata ttttgaattc ctgagttcat ccatccctag ttgttaatcg acttatgtaa 600
 aggatttgct tcatcaagct tttgcaagat ctacagtgtg atgaatcaga acacagctat 660
 ccagagagct cactctaaac taaatcaatc cctttagaat ggttctctgt ttcactaact 720
 tttttttaat gtcattttta ttatagattc ttgtgttatt tacaggccaa gtgagagtga 780
 atg gtt ctg aag atg ggc ccg gta ggt gca gag gca gat gag aat caa 828
 Met Val Leu Lys Met Gly Pro Val Gly Ala Glu Ala Asp Glu Asn Gln
 1 5 10 15
 act gta gaa gtg aaa gtg gag ccc tat ggg cca ggg cac act act cct 876
 Thr Val Glu Val Lys Val Glu Pro Tyr Gly Pro Gly His Thr Thr Pro
 20 25 30
 aga ggt gag ttg ccc cct gat ccg gag ccg gag ctc ata gac agc acc 924

Arg	Gly	Glu	Leu	Pro	Pro	Asp	Pro	Glu	Pro	Glu	Leu	Ile	Asp	Ser	Thr	
		35					40					45				
aaa	ctg	gtc	gag	gtg	cag	gtg	atc	ctc	ata	ttg	gcc	tac	tgc	tcc	atc	972
Lys	Leu	Val	Glu	Val	Gln	Val	Ile	Leu	Ile	Leu	Ala	Tyr	Cys	Ser	Ile	
		50				55					60					
atc	ttg	cta	ggg	gta	gtt	ggc	aac	tcc	ctg	gta	atc	cat	gtg	gta	atc	1020
Ile	Leu	Leu	Gly	Val	Val	Gly	Asn	Ser	Leu	Val	Ile	His	Val	Val	Ile	
		65			70					75					80	
aaa	ttc	aag	agc	atg	cgc	aca	gta	acc	aac	ttt	ttt	att	gcc	aac	ctg	1068
Lys	Phe	Lys	Ser	Met	Arg	Thr	Val	Thr	Asn	Phe	Phe	Ile	Ala	Asn	Leu	
				85					90					95		
gct	gtg	gcg	gat	ctt	ttg	gtg	aac	acc	ctg	tgc	ctg	cca	ttc	act	ctt	1116
Ala	Val	Ala	Asp	Leu	Leu	Val	Asn	Thr	Leu	Cys	Leu	Pro	Phe	Thr	Leu	
			100					105					110			
acc	tat	acc	ttg	atg	gga	gag	tgg	aaa	atg	ggt	ccg	gtc	ttg	tgc	cat	1164
Thr	Tyr	Thr	Leu	Met	Gly	Glu	Trp	Lys	Met	Gly	Pro	Val	Leu	Cys	His	
		115					120					125				
ttg	gtg	ccc	tat	gcc	cag	ggt	ctg	gcg	gta	caa	gtg	tcc	aca	ata	act	1212
Leu	Val	Pro	Tyr	Ala	Gln	Gly	Leu	Ala	Val	Gln	Val	Ser	Thr	Ile	Thr	
		130				135					140					
ttg	aca	gtc	att	gct	ctg	gac	cgc	cat	cgt	tgc	att	gtc	tac	cac	ctg	1260
Leu	Thr	Val	Ile	Ala	Leu	Asp	Arg	His	Arg	Cys	Ile	Val	Tyr	His	Leu	
		145			150					155					160	
gag	agc	aag	atc	tcc	aag	cga	atc	agc	ttc	ctg	atc	att	ggc	ctg	gcc	1308
Glu	Ser	Lys	Ile	Ser	Lys	Arg	Ile	Ser	Phe	Leu	Ile	Ile	Gly	Leu	Ala	
				165					170					175		
tgg	ggc	atc	agc	gct	ctg	ctg	gca	agt	cca	ctg	gcc	atc	ttc	cgg	gaa	1356
Trp	Gly	Ile	Ser	Ala	Leu	Leu	Ala	Ser	Pro	Leu	Ala	Ile	Phe	Arg	Glu	
			180					185					190			
tac	tcc	ctg	att	gag	atc	att	cct	gac	ttt	gag	att	gtg	gcc	tgt	acc	1404
Tyr	Ser	Leu	Ile	Glu	Ile	Ile	Pro	Asp	Phe	Glu	Ile	Val	Ala	Cys	Thr	
		195					200					205				
gag	aag	tgg	cct	ggg	gaa	gag	aag	agt	gtg	tat	ggt	aca	gtc	tac	agc	1452
Glu	Lys	Trp	Pro	Gly	Glu	Glu	Lys	Ser	Val	Tyr	Gly	Thr	Val	Tyr	Ser	
		210				215					220					
ctt	tcc	acc	ctg	ctc	atc	ctg	tac	gtt	ttg	cct	ctg	ggc	atc	ata	tct	1500
Leu	Ser	Thr	Leu	Leu	Ile	Leu	Tyr	Val	Leu	Pro	Leu	Gly	Ile	Ile	Ser	
		225			230					235					240	
ttc	tcc	tac	acc	cgt	atc	tgg	agt	aag	ctg	agg	aac	cac	gtc	agt	cct	1548
Phe	Ser	Tyr	Thr	Arg	Ile	Trp	Ser	Lys	Leu	Arg	Asn	His	Val	Ser	Pro	
				245					250					255		
gga	gct	gca	agt	gac	cat	tac	cat	cag	cga	agg	cac	aaa	atg	acc	aaa	1596
Gly	Ala	Ala	Ser	Asp	His	Tyr	His	Gln	Arg	Arg	His	Lys	Met	Thr	Lys	
			260					265					270			
atg	ctg	gtg	tgc	gtg	gta	gtg	gtg	ttt	gca	gtc	agc	tgg	cta	ccc	ctc	1644

Met	Leu	Val	Cys	Val	Val	Val	Val	Phe	Ala	Val	Ser	Trp	Leu	Pro	Leu		
	275						280					285					
cac	gcc	ttc	caa	ctc	gct	gtg	gac	atc	gac	agc	cac	gtc	ctg	gac	ctg		1692
His	Ala	Phe	Gln	Leu	Ala	Val	Asp	Ile	Asp	Ser	His	Val	Leu	Asp	Leu		
	290					295					300						
aag	gag	tac	aaa	ctc	atc	ttc	acc	gtg	ttc	cac	att	atc	gcc	atg	tgc		1740
Lys	Glu	Tyr	Lys	Leu	Ile	Phe	Thr	Val	Phe	His	Ile	Ile	Ala	Met	Cys		
	305				310					315					320		
tcc	acc	ttt	gcc	aac	ccc	ctt	ctc	tat	ggc	tgg	atg	aat	agc	aac	tac		1788
Ser	Thr	Phe	Ala	Asn	Pro	Leu	Leu	Tyr	Gly	Trp	Met	Asn	Ser	Asn	Tyr		
				325						330					335		
aga	aaa	gct	ttc	ctc	tcg	gcc	ttc	cgc	tgt	gag	cag	agg	ttg	gat	gcc		1836
Arg	Lys	Ala	Phe	Leu	Ser	Ala	Phe	Arg	Cys	Glu	Gln	Arg	Leu	Asp	Ala		
			340					345					350				
att	cac	tcg	gag	gtg	tct	atg	acc	ttc	aag	gct	aaa	aag	aac	ctg	gaa		1884
Ile	His	Ser	Glu	Val	Ser	Met	Thr	Phe	Lys	Ala	Lys	Lys	Asn	Leu	Glu		
		355				360						365					
gtc	aaa	aag	aac	aat	ggc	ccc	act	gac	tct	ttt	tcg	gag	gct	acc	aat		1932
Val	Lys	Lys	Asn	Asn	Gly	Pro	Thr	Asp	Ser	Phe	Ser	Glu	Ala	Thr	Asn		
	370				375						380						
gtg	taa	ggacacaggt	gtgaaagcac	atgggtgaat	tgtaaccagc	gctgccaatc											1988
Val																	
	385																
tggttaggga	aggttttctg	gccagtgcac	gcagacctcc	cattgtattg	actcaaaaag												2048
caacagaacc	gaagccccag	cagttttatt	tctggaaaac	tggctggcag	aaggaggtaa												2108
aaataaacag	attgccatgg	cacaacgttc	tgattaccga	tgcttggatt	gtaggttgaa												2168
ttatgagtag	agaaggggaag	gaaaacagaa	caaggagttg	gcaccagcat	ggttaaaagg												2228
gagaagtaag	tgttatctct	gagagcacag	taggatctgc	atcaggcaca	ctgtggactc												2288
catgggctcc	ctcatcactt	gatgaaaagc	tgctaaacaa	ctcagatttc	cctagggagc												2348
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agaataaaca	catttgctat	acgagtaatg	ttttggcaat	gatgggagag	attcttatat												2528
aatcagtgag	caattagttg	ttgttcagat	caaatgcact	actgttgaaa	gtttgttttt												2588
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tt																	2650

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<400> 14

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Arg Gly Glu Leu Pro Pro Asp Pro Glu Pro Glu Leu Ile Asp Ser Thr
35 40 45

Lys Leu Val Glu Val Gln Val Ile Leu Ile Leu Ala Tyr Cys Ser Ile
50 55 60

Ile Leu Leu Gly Val Val Gly Asn Ser Leu Val Ile His Val Val Ile
65 70 75 80

Lys Phe Lys Ser Met Arg Thr Val Thr Asn Phe Phe Ile Ala Asn Leu
85 90 95

Ala Val Ala Asp Leu Leu Val Asn Thr Leu Cys Leu Pro Phe Thr Leu
100 105 110

Thr Tyr Thr Leu Met Gly Glu Trp Lys Met Gly Pro Val Leu Cys His
115 120 125

Leu Val Pro Tyr Ala Gln Gly Leu Ala Val Gln Val Ser Thr Ile Thr
130 135 140

Leu Thr Val Ile Ala Leu Asp Arg His Arg Cys Ile Val Tyr His Leu
145 150 155 160

Glu Ser Lys Ile Ser Lys Arg Ile Ser Phe Leu Ile Ile Gly Leu Ala
165 170 175

Trp Gly Ile Ser Ala Leu Leu Ala Ser Pro Leu Ala Ile Phe Arg Glu
180 185 190

Tyr Ser Leu Ile Glu Ile Ile Pro Asp Phe Glu Ile Val Ala Cys Thr
195 200 205

Glu Lys Trp Pro Gly Glu Glu Lys Ser Val Tyr Gly Thr Val Tyr Ser
210 215 220

Leu Ser Thr Leu Leu Ile Leu Tyr Val Leu Pro Leu Gly Ile Ile Ser

225		230		235		240
Phe Ser Tyr Thr Arg Ile Trp Ser Lys Leu Arg Asn His Val Ser Pro						
	245			250		255
Gly Ala Ala Ser Asp His Tyr His Gln Arg Arg His Lys Met Thr Lys						
	260			265		270
Met Leu Val Cys Val Val Val Val Phe Ala Val Ser Trp Leu Pro Leu						
	275			280		285
His Ala Phe Gln Leu Ala Val Asp Ile Asp Ser His Val Leu Asp Leu						
	290			295		300
Lys Glu Tyr Lys Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys						
305		310		315		320
Ser Thr Phe Ala Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr						
	325			330		335
Arg Lys Ala Phe Leu Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala						
	340			345		350
Ile His Ser Glu Val Ser Met Thr Phe Lys Ala Lys Lys Asn Leu Glu						
	355			360		365
Val Lys Lys Asn Asn Gly Pro Thr Asp Ser Phe Ser Glu Ala Thr Asn						
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Val						
385						

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gagttccatt tgtttgttt gcaggctgca tctctgaagt aggcccttta ctctggagat	180

tccccgatct tctcacacct acc atg aat acc tct cat ttc ttg gcc cct ctc	233
Met Asn Thr Ser His Phe Leu Ala Pro Leu	
1 5 10	
ttc cca gga tcc cta cag ggt aag aat ggg acc aat cca ttg gat tcc	281
Phe Pro Gly Ser Leu Gln Gly Lys Asn Gly Thr Asn Pro Leu Asp Ser	
15 20 25	
ccc tat aat ttc tct gat ggc tgc cag gat tcg gca gaa ctg ttg gcc	329
Pro Tyr Asn Phe Ser Asp Gly Cys Gln Asp Ser Ala Glu Leu Leu Ala	
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ttc atc atc acc acc tac agc att gag acc atc tta ggg gtc ctg gga	377
Phe Ile Ile Thr Thr Tyr Ser Ile Glu Thr Ile Leu Gly Val Leu Gly	
45 50 55	
aac ctc tgc ttg ata ttt gtg acc aca aga caa aag gaa aag tcc aat	425
Asn Leu Cys Leu Ile Phe Val Thr Thr Arg Gln Lys Glu Lys Ser Asn	
60 65 70	
gtg acc aac cta ctc att gcc aac ctg gcc ttc tct gac ttc ctc atg	473
Val Thr Asn Leu Leu Ile Ala Asn Leu Ala Phe Ser Asp Phe Leu Met	
75 80 85 90	
tgc ctc atc tgc caa cca ctc aca gtc acc tac acc atc atg gat tac	521
Cys Leu Ile Cys Gln Pro Leu Thr Val Thr Tyr Thr Ile Met Asp Tyr	
95 100 105	
tgg atc ttt ggt gaa gtc ctt tgc aag atg tta act ttc atc cag tgt	569
Trp Ile Phe Gly Glu Val Leu Cys Lys Met Leu Thr Phe Ile Gln Cys	
110 115 120	
atg tca gtg aca gtc tcc atc ctc tca ctg gtc ctt gtg gcc ctg gag	617
Met Ser Val Thr Val Ser Ile Leu Ser Leu Val Leu Val Ala Leu Glu	
125 130 135	
aga cac cag ctc att atc aat cca aca ggc tgg aaa ccc agt att ttc	665
Arg His Gln Leu Ile Ile Asn Pro Thr Gly Trp Lys Pro Ser Ile Phe	
140 145 150	
cag gcc tac ctg ggg att gtg gtc atc tgg ttc atc tct tgt ttc ctt	713
Gln Ala Tyr Leu Gly Ile Val Val Ile Trp Phe Ile Ser Cys Phe Leu	
155 160 165 170	
tcc ttg ccg ttc ctg gcc aac agc acc ctg aat gac ctc ttc cac tac	761
Ser Leu Pro Phe Leu Ala Asn Ser Thr Leu Asn Asp Leu Phe His Tyr	
175 180 185	
aac cac tct aag gtt gta gag ttt ctg gaa gac aag gtc gtc tgc ttt	809
Asn His Ser Lys Val Val Glu Phe Leu Glu Asp Lys Val Val Cys Phe	
190 195 200	
gtg tcc tgg tct tca gat cac cac cgt ctc atc tat acc acc ttt ctg	857
Val Ser Trp Ser Ser Asp His His Arg Leu Ile Tyr Thr Thr Phe Leu	
205 210 215	
ctg ctc ttt cag tac tgc atc cct cta gcc ttc atc ctg gtc tgc tac	905
Leu Leu Phe Gln Tyr Cys Ile Pro Leu Ala Phe Ile Leu Val Cys Tyr	
220 225 230	

ata cgc atc tac cag cgc ctg cag agg cag aag cat gtg ttc cat gcg	953
Ile Arg Ile Tyr Gln Arg Leu Gln Arg Gln Lys His Val Phe His Ala	
235 240 245 250	
cac gct tgc agc tca cga gcg ggg cag atg aag cgg atc aac agc atg	1001
His Ala Cys Ser Ser Arg Ala Gly Gln Met Lys Arg Ile Asn Ser Met	
255 260 265	
ctc atg aca atg gtg act gcc ttt gca gtt ctc tgg cta ccc ctg cat	1049
Leu Met Thr Met Val Thr Ala Phe Ala Val Leu Trp Leu Pro Leu His	
270 275 280	
gtg ttc aac act ctg gag gac tgg tac cag gaa gcc atc cct gct tgc	1097
Val Phe Asn Thr Leu Glu Asp Trp Tyr Gln Glu Ala Ile Pro Ala Cys	
285 290 295	
cat ggc aac ctc atc ttc ttg atg tgc cac ctg ttg gcc atg gct tcc	1145
His Gly Asn Leu Ile Phe Leu Met Cys His Leu Leu Ala Met Ala Ser	
300 305 310	
acc tgt gtc aac cct ttc atc tat ggc ttt ctc aac atc aac ttc aag	1193
Thr Cys Val Asn Pro Phe Ile Tyr Gly Phe Leu Asn Ile Asn Phe Lys	
315 320 325 330	
aag gat atc aag gct ctg gtg ctg acc tgc cat tgc agg tca cct caa	1241
Lys Asp Ile Lys Ala Leu Val Leu Thr Cys His Cys Arg Ser Pro Gln	
335 340 345	
ggg gag tct gag cat ctg ccc ctg tcc act gtt cac acg gac ctc tcc	1289
Gly Glu Ser Glu His Leu Pro Leu Ser Thr Val His Thr Asp Leu Ser	
350 355 360	
aag gga tcg atg agg atg ggt agc aag tct aac ttc ata tag	1331
Lys Gly Ser Met Arg Met Gly Ser Lys Ser Asn Phe Ile	
365 370 375	
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cacattgcag gctgtgatag catcctgtca tttctggcctt ttggggccca gatagggttg	1451
caagagactt gaagccttggc attcagatgg tttagccctt tgcttctgag agatctctga	1511
gtcaggattc tgcagatcac agagggaact ttgtggccttg agctgcaagg gtattagagt	1571
cagaagtggc tgactctcac agccactcag tacagatgcc tggcccaaaa gccttcatct	1631
atgtcctgac cattcagcta acctgccttt ggtgatgtgc ttatgttctt ccaagggatg	1691
ttgggtgttt cagtatgg	1709

<210> 16
 <211> 375
 <212> PRT
 <213> mouse neuropeptide Y4 receptor

<400> 16

Met Asn Thr Ser His Phe Leu Ala Pro Leu Phe Pro Gly Ser Leu Gln
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Gly Lys Asn Gly Thr Asn Pro Leu Asp Ser Pro Tyr Asn Phe Ser Asp
 20 25 30
 Gly Cys Gln Asp Ser Ala Glu Leu Leu Ala Phe Ile Ile Thr Thr Tyr
 35 40 45
 Ser Ile Glu Thr Ile Leu Gly Val Leu Gly Asn Leu Cys Leu Ile Phe
 50 55 60
 Val Thr Thr Arg Gln Lys Glu Lys Ser Asn Val Thr Asn Leu Leu Ile
 65 70 75 80
 Ala Asn Leu Ala Phe Ser Asp Phe Leu Met Cys Leu Ile Cys Gln Pro
 85 90 95
 Leu Thr Val Thr Tyr Thr Ile Met Asp Tyr Trp Ile Phe Gly Glu Val
 100 105 110
 Leu Cys Lys Met Leu Thr Phe Ile Gln Cys Met Ser Val Thr Val Ser
 115 120 125
 Ile Leu Ser Leu Val Leu Val Ala Leu Glu Arg His Gln Leu Ile Ile
 130 135 140
 Asn Pro Thr Gly Trp Lys Pro Ser Ile Phe Gln Ala Tyr Leu Gly Ile
 145 150 155 160
 Val Val Ile Trp Phe Ile Ser Cys Phe Leu Ser Leu Pro Phe Leu Ala
 165 170 175
 Asn Ser Thr Leu Asn Asp Leu Phe His Tyr Asn His Ser Lys Val Val
 180 185 190
 Glu Phe Leu Glu Asp Lys Val Val Cys Phe Val Ser Trp Ser Ser Asp
 195 200 205
 His His Arg Leu Ile Tyr Thr Thr Phe Leu Leu Leu Phe Gln Tyr Cys
 210 215 220
 Ile Pro Leu Ala Phe Ile Leu Val Cys Tyr Ile Arg Ile Tyr Gln Arg
 225 230 235 240
 Leu Gln Arg Gln Lys His Val Phe His Ala His Ala Cys Ser Ser Arg
 245 250 255

Ala Gly Gln Met Lys Arg Ile Asn Ser Met Leu Met Thr Met Val Thr
 260 265 270

Ala Phe Ala Val Leu Trp Leu Pro Leu His Val Phe Asn Thr Leu Glu
 275 280 285

Asp Trp Tyr Gln Glu Ala Ile Pro Ala Cys His Gly Asn Leu Ile Phe
 290 295 300

Leu Met Cys His Leu Leu Ala Met Ala Ser Thr Cys Val Asn Pro Phe
 305 310 315 320

Ile Tyr Gly Phe Leu Asn Ile Asn Phe Lys Lys Asp Ile Lys Ala Leu
 325 330 335

Val Leu Thr Cys His Cys Arg Ser Pro Gln Gly Glu Ser Glu His Leu
 340 345 350

Pro Leu Ser Thr Val His Thr Asp Leu Ser Lys Gly Ser Met Arg Met
 355 360 365

Gly Ser Lys Ser Asn Phe Ile
 370 375

<210> 17
 <211> 1868
 <212> DNA
 <213> mouse neuropeptide Y5 receptor

<220>
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 Met Glu Val Lys Leu
 1 5
 gaa gag cat ttt aac aag aca ttt gtc acg gag aac aat act gct gcc 162
 Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu Asn Asn Thr Ala Ala
 10 15 20
 agt cag aac acg gcc tcc cct gcc tgg gag gac tac aga ggc aca gag 210
 Ser Gln Asn Thr Ala Ser Pro Ala Trp Glu Asp Tyr Arg Gly Thr Glu
 25 30 35
 aac aat act tct gct gct cgg aac act gcc ttt cca gtc tgg gag gac 258

Asn	Asn	Thr	Ser	Ala	Ala	Arg	Asn	Thr	Ala	Phe	Pro	Val	Trp	Glu	Asp	
	40						45					50				
tat	aga	ggc	agc	gta	gac	gac	tta	caa	tac	ttc	ctg	att	ggg	ctc	tat	306
Tyr	Arg	Gly	Ser	Val	Asp	Asp	Leu	Gln	Tyr	Phe	Leu	Ile	Gly	Leu	Tyr	
	55					60					65					
aca	ttt	gta	agt	ctt	ctt	ggg	ttt	atg	gga	aat	cta	ctt	atc	tta	atg	354
Thr	Phe	Val	Ser	Leu	Leu	Gly	Phe	Met	Gly	Asn	Leu	Leu	Ile	Leu	Met	
	70				75					80					85	
gct	gtt	atg	aaa	aag	cgc	aat	cag	aag	act	aca	gtg	aac	ttt	ctc	ata	402
Ala	Val	Met	Lys	Lys	Arg	Asn	Gln	Lys	Thr	Val	Val	Asn	Phe	Leu	Ile	
				90					95					100		
ggc	aac	ctg	gcc	ttc	tcc	gac	att	ttg	gtt	gtc	ctg	ttt	tgc	tcc	cct	450
Gly	Asn	Leu	Ala	Phe	Ser	Asp	Ile	Leu	Val	Val	Leu	Phe	Cys	Ser	Pro	
			105					110					115			
ttc	acc	ctg	acc	tct	gtc	ttg	ttg	gat	cag	tgg	atg	ttc	ggc	aaa	gcc	498
Phe	Thr	Leu	Thr	Ser	Val	Leu	Leu	Asp	Gln	Trp	Met	Phe	Gly	Lys	Ala	
		120					125					130				
atg	tgc	cat	atc	atg	cca	ttc	ctt	cag	tgt	gta	tca	gtt	ctg	gtt	tca	546
Met	Cys	His	Ile	Met	Pro	Phe	Leu	Gln	Cys	Val	Ser	Val	Leu	Val	Ser	
	135					140					145					
act	ctg	att	tta	ata	tcg	att	gcc	att	gtc	agg	tat	cat	atg	ata	aag	594
Thr	Leu	Ile	Leu	Ile	Ser	Ile	Ala	Ile	Val	Arg	Tyr	His	Met	Ile	Lys	
	150					155				160					165	
cac	cct	ata	tct	aac	aat	tta	aca	gca	aac	cat	ggc	tac	ttc	ctg	ata	642
His	Pro	Ile	Ser	Asn	Asn	Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile	
				170					175					180		
gct	act	gtc	tgg	aca	ctg	ggc	ttt	gcc	atc	tgt	tct	ccc	ctc	cca	gtg	690
Ala	Thr	Val	Trp	Thr	Leu	Gly	Phe	Ala	Ile	Cys	Ser	Pro	Leu	Pro	Val	
			185					190					195			
ttt	cac	agc	ctt	gtg	gaa	ctt	aag	gaa	acc	ttt	ggc	tca	gca	ttg	cta	738
Phe	His	Ser	Leu	Val	Glu	Leu	Lys	Glu	Thr	Phe	Gly	Ser	Ala	Leu	Leu	
		200					205					210				
agc	agc	aag	tat	ttg	tgt	gtt	gag	tca	tgg	ccc	tct	gat	tca	tac	aga	786
Ser	Ser	Lys	Tyr	Leu	Cys	Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg	
	215					220					225					
att	gct	ttc	aca	atc	tct	tta	ttg	tta	gtt	cag	tat	atc	ctg	cct	cta	834
Ile	Ala	Phe	Thr	Ile	Ser	Leu	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu	
	230				235					240					245	
gta	tgt	tta	aca	gta	agt	cat	act	agt	gtc	tgc	agg	agt	ata	agc	tgt	882
Val	Cys	Leu	Thr	Val	Ser	His	Thr	Ser	Val	Cys	Arg	Ser	Ile	Ser	Cys	
				250					255					260		
gga	ttg	tcc	cac	aaa	gaa	aac	aga	ctc	gaa	gaa	aat	gag	atg	atc	aac	930
Gly	Leu	Ser	His	Lys	Glu	Asn	Arg	Leu	Glu	Glu	Asn	Glu	Met	Ile	Asn	
			265					270					275			
tta	act	cta	cat	cca	tcc	aaa	aag	agt	cgg	gac	cag	gca	aaa	ccc	ccc	978

Leu Thr Leu His Pro Ser Lys Lys Ser Arg Asp Gln Ala Lys Pro Pro	
280 285 290	
agc act caa aag tgg agc tac tca ttc atc aga aag cac cga aga agg	1026
Ser Thr Gln Lys Trp Ser Tyr Ser Phe Ile Arg Lys His Arg Arg Arg	
295 300 305	
tac agc aag aag acg gca tgc gtg tta ccc gcc cca gca gga cct tcc	1074
Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala Pro Ala Gly Pro Ser	
310 315 320 325	
cag gag aag cac cta acc gtt cca gaa aac cca ggc tcg gtc cgt agc	1122
Gln Glu Lys His Leu Thr Val Pro Glu Asn Pro Gly Ser Val Arg Ser	
330 335 340	
cag ctg tca cca tcc agt aag gtt att cca ggg gtc ccg atc tgc ttt	1170
Gln Leu Ser Pro Ser Ser Lys Val Ile Pro Gly Val Pro Ile Cys Phe	
345 350 355	
gag gtg aaa cct gaa gaa agc tca gat gct cag gag atg aga gtc aag	1218
Glu Val Lys Pro Glu Glu Ser Ser Asp Ala Gln Glu Met Arg Val Lys	
360 365 370	
cgt tcc ctc acg aga ata aag aag aga tct cgc agt gtt ttc tac aga	1266
Arg Ser Leu Thr Arg Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg	
375 380 385	
ctg act ata ttg ata tta gtg ttc gct gtt agc tgg atg cca ctc cac	1314
Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro Leu His	
390 395 400 405	
gtc ttc cac gtg gtg acc gat ttc aat gat aac ctg att tcc aat agg	1362
Val Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg	
410 415 420	
cat ttc aag ctg gtg tac tgc atc tgt cac ttg tta ggc atg atg tcc	1410
His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser	
425 430 435	
tgt tgt ctt aat ccg atc tta tat gga ttc ctt aat aat ggt atc aaa	1458
Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Lys	
440 445 450	
gca gac ttg aga gcc ctt atc cac tgc cta cac atg tca tga	1500
Ala Asp Leu Arg Ala Leu Ile His Cys Leu His Met Ser	
455 460 465	
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attgatgcat aatttacata aacgtgttct ggatctgaat gccagtttgt aatctatgta	1620
agatcattta tgttataatg tggttaattc cgtcacttgt gcagagtcaa tgtcgatcta	1680
aggaaatttc tgtcttgaaa tagttacatt accgtccatt tcatgtcatt ggtaataagt	1740
tgagtgtctt cggtttcgag taaaagttat agctatccaa attgttattt tgtacaaaaa	1800
tgtgaagaagt gaaaaagttg ttccaaagaa tattttaacct cagatttaag gaatttcctt	1860
tatctaga	1868

<210> 18
 <211> 466
 <212> PRT
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<400> 18

Met Glu Val Lys Leu Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu
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Asn Asn Thr Ala Ala Ser Gln Asn Thr Ala Ser Pro Ala Trp Glu Asp
 20 25 30

Tyr Arg Gly Thr Glu Asn Asn Thr Ser Ala Ala Arg Asn Thr Ala Phe
 35 40 45

Pro Val Trp Glu Asp Tyr Arg Gly Ser Val Asp Asp Leu Gln Tyr Phe
 50 55 60

Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn
 65 70 75 80

Leu Leu Ile Leu Met Ala Val Met Lys Lys Arg Asn Gln Lys Thr Thr
 85 90 95

Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val
 100 105 110

Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp
 115 120 125

Met Phe Gly Lys Ala Met Cys His Ile Met Pro Phe Leu Gln Cys Val
 130 135 140

Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg
 145 150 155 160

Tyr His Met Ile Lys His Pro Ile Ser Asn Asn Leu Thr Ala Asn His
 165 170 175

Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys
 180 185 190

Ser Pro Leu Pro Val Phe His Ser Leu Val Glu Leu Lys Glu Thr Phe
 195 200 205

Gly Ser Ala Leu Leu Ser Ser Lys Tyr Leu Cys Val Glu Ser Trp Pro
210 215 220

Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln
225 230 235 240

Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser His Thr Ser Val Cys
245 250 255

Arg Ser Ile Ser Cys Gly Leu Ser His Lys Glu Asn Arg Leu Glu Glu
260 265 270

Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser Lys Lys Ser Arg Asp
275 280 285

Gln Ala Lys Pro Pro Ser Thr Gln Lys Trp Ser Tyr Ser Phe Ile Arg
290 295 300

Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala
305 310 315 320

Pro Ala Gly Pro Ser Gln Glu Lys His Leu Thr Val Pro Glu Asn Pro
325 330 335

Gly Ser Val Arg Ser Gln Leu Ser Pro Ser Ser Lys Val Ile Pro Gly
340 345 350

Val Pro Ile Cys Phe Glu Val Lys Pro Glu Glu Ser Ser Asp Ala Gln
355 360 365

Glu Met Arg Val Lys Arg Ser Leu Thr Arg Ile Lys Lys Arg Ser Arg
370 375 380

Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser
385 390 395 400

Trp Met Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn
405 410 415

Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu
420 425 430

Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu
435 440 445

Asn Asn Gly Ile Lys Ala Asp Leu Arg Ala Leu Ile His Cys Leu His
 450 455 460

Met Ser
 465

<210> 19
 <211> 2281
 <212> DNA
 <213> mouse neuropeptide y6 receptor

<220>
 <221> CDS
 <222> (823)..(1938)

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 cttcgtttac tgcttctgaa gcctatactg atagaattaa taaaatactg agagagagag 180
 agagggacag agagagagag ggggagagag agagagagag agagagagag agagagagag 240
 agagagagag agaagagaag aaaacaaggt saagccatct gcttaactta tgtccacatt 300
 ctctcaagag cattgtccta tttgtagaat tatctatatt gttaagaatc atctccattg 360
 ttaagatttt gtgggctgga gatccagctc tgttgataaaa gtgcttgcct aacatgcatg 420
 aagtcctagg ttctattccc aaggctacat aaaaccttgt gttgtgatga atgcctgtaa 480
 tcccagtacg cagcaaggag agacaaggag gatcagaagc ttaaggacat cattttgtac 540
 atagtgagtt tgaggaaagc tgaggttaca tggaaactctc tctctctcaa aaacaaaaca 600
 aaacaaaaca aaaccttcta ctaatatctt ggattctggt tgatttttag gatctcaaga 660
 gcatgctgac gtcatttatg tgtttccatc agatacagac agagatcata aacatttaac 720
 tcattgatta tatgttgaga gttgtccctc aagaaccaat ggccaaacat ccactgagga 780
 tacacggaag cttagaaaat ctctaattaa aatcctgaca ta atg gaa gtg ctc 834
 Met Glu Val Leu
 1
 aca aac cag cca aca cct aat aaa acc agt ggc aag agc aac aac tcg 882
 Thr Asn Gln Pro Thr Pro Asn Lys Thr Ser Gly Lys Ser Asn Asn Ser
 5 10 15 20
 gca ttt ttc tac ttt gaa tcc tgc caa ccc cct ttt cta gcc ata ctc 930
 Ala Phe Phe Tyr Phe Glu Ser Cys Gln Pro Pro Phe Leu Ala Ile Leu
 25 30 35
 ttg cta ctc ata gca tat act gtg atc cta atc atg ggc att ttt gga 978
 Leu Leu Leu Ile Ala Tyr Thr Val Ile Leu Ile Met Gly Ile Phe Gly

40										45										50										
aac	ctc	tct	ctt	atc	atc	atc	atc	ttt	aag	aaa	cag	aga	gaa	gct	caa	1026														
Asn	Leu	Ser	Leu	Ile	Ile	Ile	Ile	Phe	Lys	Lys	Gln	Arg	Glu	Ala	Gln															
		55					60					65																		
aat	gtt	acc	aac	ata	ctg	att	gcc	aac	ctg	tcc	ctc	tct	gac	atc	ttg	1074														
Asn	Val	Thr	Asn	Ile	Leu	Ile	Ala	Asn	Leu	Ser	Leu	Ser	Asp	Ile	Leu															
	70					75					80																			
gtg	tgt	gtc	atg	tgc	atc	cct	ttt	acg	gtc	atc	tac	act	ctg	atg	gac	1122														
Val	Cys	Val	Met	Cys	Ile	Pro	Phe	Thr	Val	Ile	Tyr	Thr	Leu	Met	Asp															
85					90					95					100															
cac	tgg	gta	ttt	ggg	aac	act	atg	tgt	aaa	ctc	act	tcc	tac	gtg	caa	1170														
His	Trp	Val	Phe	Gly	Asn	Thr	Met	Cys	Lys	Leu	Thr	Ser	Tyr	Val	Gln															
				105					110					115																
agt	gtc	tca	gtt	tct	gtg	tcc	ata	ttc	tcc	ctt	gtg	ttg	att	gct	att	1218														
Ser	Val	Ser	Val	Ser	Val	Ser	Ile	Phe	Ser	Leu	Val	Leu	Ile	Ala	Ile															
			120					125					130																	
gaa	cga	tat	cag	ctg	att	gtg	aac	ccc	cgt	ggc	tgg	aaa	ccc	aga	gta	1266														
Glu	Arg	Tyr	Gln	Leu	Ile	Val	Asn	Pro	Arg	Gly	Trp	Lys	Pro	Arg	Val															
		135					140					145																		
gct	cat	gcc	tat	tgg	ggg	atc	atc	ttg	att	tgg	ctc	att	tct	ctg	aca	1314														
Ala	His	Ala	Tyr	Trp	Gly	Ile	Ile	Leu	Ile	Trp	Leu	Ile	Ser	Leu	Thr															
	150					155					160																			
ttg	tct	att	ccc	tta	ttc	ctg	tcc	tac	cac	ctc	acc	aat	gag	ccc	ttt	1362														
Leu	Ser	Ile	Pro	Leu	Phe	Leu	Ser	Tyr	His	Leu	Thr	Asn	Glu	Pro	Phe															
165					170					175					180															
cat	aat	ctc	tct	ctc	cct	act	gac	atc	tac	acc	cac	cag	gta	gct	tgt	1410														
His	Asn	Leu	Ser	Leu	Pro	Thr	Asp	Ile	Tyr	Thr	His	Gln	Val	Ala	Cys															
				185					190					195																
gtg	gag	att	tgg	cct	tct	aaa	ctg	aac	caa	ctc	ctc	ttt	tct	aca	tca	1458														
Val	Glu	Ile	Trp	Pro	Ser	Lys	Leu	Asn	Gln	Leu	Leu	Phe	Ser	Thr	Ser															
			200					205					210																	
tta	ttt	atg	ctc	cag	tat	ttt	gtc	cct	ctg	ggc	ttc	att	ctt	atc	tgc	1506														
Leu	Phe	Met	Leu	Gln	Tyr	Phe	Val	Pro	Leu	Gly	Phe	Ile	Leu	Ile	Cys															
		215					220					225																		
tac	ctg	aag	atc	gtt	ctc	tgc	ctc	cga	aaa	aga	act	agg	cag	gtg	gac	1554														
Tyr	Leu	Lys	Ile	Val	Leu	Cys	Leu	Arg	Lys	Arg	Thr	Arg	Gln	Val	Asp															
		230				235					240																			
agg	aga	aag	gaa	aat	aag	agc	cgt	ctc	aat	gag	aac	aag	agg	gta	aat	1602														
Arg	Arg	Lys	Glu	Asn	Lys	Ser	Arg	Leu	Asn	Glu	Asn	Lys	Arg	Val	Asn															
245					250					255					260															
gtg	atg	ttg	att	tcc	atc	gta	gtg	act	ttt	gga	gcc	tgc	tgg	ttg	ccc	1650														
Val	Met	Leu	Ile	Ser	Ile	Val	Val	Thr	Phe	Gly	Ala	Cys	Trp	Leu	Pro															
				265					270					275																
ttg	aac	att	ttc	aat	gtc	atc	ttc	gac	tgg	tat	cat	gag	atg	ctg	atg	1698														
Leu	Asn	Ile	Phe	Asn	Val	Ile	Phe	Asp	Trp	Tyr	His	Glu	Met	Leu	Met															

280	285	290	
agc tgc cac cac gac ctg gta ttt gta gtt tgc cac ttg att gct atg			1746
Ser Cys His His Asp Leu Val Phe Val Val Cys His Leu Ile Ala Met			
295	300	305	
gtt tct act tgc ata aat cct ctc ttt tat gga ttt ctc aac aaa aac			1794
Val Ser Thr Cys Ile Asn Pro Leu Phe Tyr Gly Phe Leu Asn Lys Asn			
310	315	320	
ttc cag aag gat cta atg atg ctt att cac cac tgt tgg tgt ggt gaa			1842
Phe Gln Lys Asp Leu Met Met Leu Ile His His Cys Trp Cys Gly Glu			
325	330	335	340
cct cag gaa agt tat gaa aat att gcc atg tct act atg cac aca gat			1890
Pro Gln Glu Ser Tyr Glu Asn Ile Ala Met Ser Thr Met His Thr Asp			
345	350	355	
gaa tcc aag gga tca tta aaa ctg gct cac ata cca aca ggc ata tag			1938
Glu Ser Lys Gly Ser Leu Lys Leu Ala His Ile Pro Thr Gly Ile			
360	365	370	
aaactggtaa gcaaaatcaa agcccttctg ttatgaaaga aagagaagaa atagtatgga			1998
ataggggcaag gtgcagagga agccagactt aaacacataa tatctttggg cccagttttg			2058
ctttaagtta agcatgtcta ctccattcag ccatagaaca cacagagatt tatccctacc			2118
ctttcttttt ttccttttga agaataataa cttaaacaac ctagacatca ttactgagga			2178
agagaacaaa aatgagagag catacaagga cagcagagat gtctggggta caaaattcac			2238
gttattcgct ggaatagcta gaaagttatt agttgtgctg cag			2281

<210> 20
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 <212> PRT
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 <400> 20

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Leu Ala Ile Leu Leu Leu Leu Ile Ala Tyr Thr Val Ile Leu Ile Met	
35 40 45	
Gly Ile Phe Gly Asn Leu Ser Leu Ile Ile Ile Ile Phe Lys Lys Gln	
50 55 60	
Arg Glu Ala Gln Asn Val Thr Asn Ile Leu Ile Ala Asn Leu Ser Leu	
65 70 75 80	

Ser Asp Ile Leu Val Cys Val Met Cys Ile Pro Phe Thr Val Ile Tyr
85 90 95

Thr Leu Met Asp His Trp Val Phe Gly Asn Thr Met Cys Lys Leu Thr
100 105 110

Ser Tyr Val Gln Ser Val Ser Val Ser Val Ser Ile Phe Ser Leu Val
115 120 125

Leu Ile Ala Ile Glu Arg Tyr Gln Leu Ile Val Asn Pro Arg Gly Trp
130 135 140

Lys Pro Arg Val Ala His Ala Tyr Trp Gly Ile Ile Leu Ile Trp Leu
145 150 155 160

Ile Ser Leu Thr Leu Ser Ile Pro Leu Phe Leu Ser Tyr His Leu Thr
165 170 175

Asn Glu Pro Phe His Asn Leu Ser Leu Pro Thr Asp Ile Tyr Thr His
180 185 190

Gln Val Ala Cys Val Glu Ile Trp Pro Ser Lys Leu Asn Gln Leu Leu
195 200 205

Phe Ser Thr Ser Leu Phe Met Leu Gln Tyr Phe Val Pro Leu Gly Phe
210 215 220

Ile Leu Ile Cys Tyr Leu Lys Ile Val Leu Cys Leu Arg Lys Arg Thr
225 230 235 240

Arg Gln Val Asp Arg Arg Lys Glu Asn Lys Ser Arg Leu Asn Glu Asn
245 250 255

Lys Arg Val Asn Val Met Leu Ile Ser Ile Val Val Thr Phe Gly Ala
260 265 270

Cys Trp Leu Pro Leu Asn Ile Phe Asn Val Ile Phe Asp Trp Tyr His
275 280 285

Glu Met Leu Met Ser Cys His His Asp Leu Val Phe Val Val Cys His
290 295 300

Leu Ile Ala Met Val Ser Thr Cys Ile Asn Pro Leu Phe Tyr Gly Phe
305 310 315 320

Leu Asn Lys Asn Phe Gln Lys Asp Leu Met Met Leu Ile His His Cys
325 330 335

Trp Cys Gly Glu Pro Gln Glu Ser Tyr Glu Asn Ile Ala Met Ser Thr
340 345 350

Met His Thr Asp Glu Ser Lys Gly Ser Leu Lys Leu Ala His Ile Pro
355 360 365

Thr Gly Ile
370